



SEQUENCE LISTING

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The Government of the United States of America
as represented by the Secretary,
Department of Health and Human Services

<120> Pseudomonas Exotoxin A-Like Chimeric Immunogens

<130> 015280-310100US

<140> US 09/462,682

<141> 2000-04-28

<150> US 60/052,375

<151> 1997-07-11

<150> WO PCT/US98/14341

<151> 1998-07-10

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 1839

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)...(1839)

<223> exotoxin A

<400> 1

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gcc | gaa | gac | gct | tcc | gac | ctc | tgg | aac | gaa | tgc | gcc | aaa | gcc | tgc | gtg | 48 |
| Ala | Glu | Glu | Ala | Phe | Asp | Leu | Trp | Asn | Glu | Cys | Ala | Lys | Ala | Cys | Val | |
| 1 | | | | | | | | 5 | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ctc | gac | ctc | aag | gac | ggc | gtg | cgt | tcc | agc | cgc | atg | agc | gtc | gac | ccg | 96 |
| Leu | Asp | Leu | Lys | Asp | Gly | Val | Arg | Ser | Ser | Arg | Met | Ser | Val | Asp | Pro | |
| | | | | | | | | 20 | | | 25 | | | | 30 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | atc | gcc | gac | acc | aac | ggc | cag | ggc | gtg | ctg | cac | tac | tcc | atg | gtc | 144 |
| Ala | Ile | Ala | Asp | Thr | Asn | Gly | Gln | Gly | Val | Leu | His | Tyr | Ser | Met | Val | |
| | | | | | | | | 35 | | 40 | | | 45 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| ctg | gag | ggc | aac | gac | gcf | ctc | aag | ctg | gcc | atc | gac | aac | gcc | ctc | 192 | |
| Leu | Glu | Gly | Asn | Asp | Ala | Leu | Lys | Leu | Ala | Ile | Asp | Asn | Ala | Leu | | |
| | | | | | | | | 50 | | 55 | | | 60 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agc | atc | acc | agc | gac | ggc | ctg | acc | atc | cgc | ctc | gaa | ggc | ggc | gtc | gag | 240 |
| Ser | Ile | Thr | Ser | Asp | Gly | Leu | Thr | Ile | Arg | Leu | Glu | Gly | Gly | Val | Glu | |
| | | | | | | | | 65 | | 70 | | | 75 | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ccg | aac | aag | ccg | gtg | cgc | tac | agc | tac | acg | cgc | cag | ggc | cgc | ggc | agt | 288 |
| Pro | Asn | Lys | Pro | Val | Arg | Tyr | Ser | Tyr | Thr | Arg | Gln | Ala | Arg | Gly | Ser | |
| | | | | | | | | 85 | | 90 | | | 95 | | | |

| | |
|---|------|
| tgg tcg ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tcg aac Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn 100 105 110 | 336 |
| atc aag gtg ttc atc cac gaa ctg aac gcc ggc aac cag ctc agc cac Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His 115 120 125 | 384 |
| atg tcg ccg atc tac acc atc gag atg ggc gac gag ttg ctg gcg aag Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys 130 135 140 | 432 |
| ctg gcg ccg gat gcc acc ttc ttc gtc agg gcg cac gag agc aac gag Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu 145 150 155 160 | 480 |
| atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met 165 170 175 | 528 |
| gcc cag acc cag ccg ccg cgaa aag cgc tgg agc gaa tgg gcc agc Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser 180 185 190 | 576 |
| ggc aag gtg ttg tgc ctg ctc gac ccg ctg gac ggg gtc tac aac tac Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr 195 200 205 | 624 |
| ctc gcc cag caa cgc tgc aac ctc gac gat acc tgg gaa ggc aag atc Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile 210 215 220 | 672 |
| tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac atc aaa Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys 225 230 235 240 | 720 |
| ccc acg gtc atc agt cat cgc ctg cac ttt ccc gag ggc ggc agc ctg Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Ser Leu 245 250 255 | 768 |
| gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe 260 265 270 | 816 |
| acc cgt cat cgc cag ccg ccg ggc tgg gaa caa ctg gag cag tgc ggc Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly 275 280 285 | 864 |
| tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg ctg tcg Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser 290 295 300 | 912 |
| tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc ccc ggc Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly 305 310 315 320 | 960 |
| agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala 325 330 335 | 1008 |

| | | | |
|---|-----|------|-----|
| cgt ctg gcc ctg acc ctg gcc gcc gag agc gag cgc ttc gtc cg | | 1056 | |
| Arg Leu Ala Leu Thr Leu Ala Ala Glu Ser Glu Arg Phe Val Arg | | | |
| 340 | 345 | 350 | |
| cag ggc acc ggc aac gac gag gcc ggc gcg gcc aac gcc gac gtg gt | | 1104 | |
| Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val | | | |
| 355 | 360 | 365 | |
| agc ctg acc tgc ccg gtc gcc ggc ggt gaa tgc gcg ggc ccg gcg gac | | 1152 | |
| Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp | | | |
| 370 | 375 | 380 | |
| agc ggc gac gcc ctg ctg gag cgc aac tat ccc act ggc gcg gag ttc | | 1200 | |
| Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe | | | |
| 385 | 390 | 395 | 400 |
| ctc ggc gac ggc ggc gac gtc agc ttc agc acc cgc ggc acg cag aac | | 1248 | |
| Leu Gly Asp Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn | | | |
| 405 | 410 | 415 | |
| tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag gag cgc | | 1296 | |
| Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg | | | |
| 420 | 425 | 430 | |
| ggc tat gtg ttc gtc ggc tac cac ggc acc ttc ctc gaa gcg gcg caa | | 1344 | |
| Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln | | | |
| 435 | 440 | 445 | |
| agc atc gtc ttc ggc ggg gtg cgc gcg cgc agc cag gac ctc gac gcg | | 1392 | |
| Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala | | | |
| 450 | 455 | 460 | |
| atc tgg cgc ggt ttc tat atc gcc ggc gat ccg gcg ctg gcc tac ggc | | 1440 | |
| Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly | | | |
| 465 | 470 | 475 | 480 |
| tac gcc cag gac cag gaa ccc gac gca cgc ggc cgg atc cgc aac ggt | | 1488 | |
| Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly | | | |
| 485 | 490 | 495 | |
| gcc ctg ctg cgg gtc tat gtg ccg cgc tcg agc ctg ccg ggc ttc tac | | 1536 | |
| Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr | | | |
| 500 | 505 | 510 | |
| cgc acc agc ctg acc ctg gcc ggc ccg gag gcg ggc gag gtc gaa | | 1584 | |
| Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu | | | |
| 515 | 520 | 525 | |
| cgg ctg atc ggc cat ccg ctg ccg ctg cgc ctg gac gcc atc acc ggc | | 1632 | |
| Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly | | | |
| 530 | 535 | 540 | |
| ccc gag gag gaa ggc ggg cgc ctg gag acc att ctc ggc tgg ccg ctg | | 1680 | |
| Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu | | | |
| 545 | 550 | 555 | 560 |
| gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac ccg cgc | | 1728 | |
| Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg | | | |
| 565 | 570 | 575 | |

aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag 1776
 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
 580 585 590

gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa ccg ccg 1824
 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
 595 600 605

cgc gag gac ctg aag 1839
 Arg Glu Asp Leu Lys
 610

<210> 2
<211> 613
<212> PRT
<213> Pseudomonas aeruginosa

<400> 2
Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
 1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
 20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
 35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
 50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
 65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
 85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
 100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
 115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
 130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
 145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
 165 170 175

Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
 180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
 195 200 205

Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
 210 215 220

Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
 225 230 235 240
 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
 245 250 255
 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
 260 265 270
 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
 275 280 285
 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
 290 295 300
 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
 305 310 315 320
 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
 325 330 335
 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
 340 345 350
 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
 355 360 365
 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
 370 375 380
 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe
 385 390 395 400
 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
 405 410 415
 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
 420 425 430
 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
 435 440 445
 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
 450 455 460
 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
 465 470 475 480
 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
 485 490 495
 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
 500 505 510
 Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
 515 520 525
 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
 530 535 540

Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
 545 550 555 560

Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
 565 570 575

Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
 580 585 590

Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
 595 600 605

Arg Glu Asp Leu Lys
 610

<210> 3
 <211> 35
 <212> PRT
 <213> Human immunodeficiency virus type 1

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> V3 loop of MN strain of HIV-1

<400> 3
 Cys Thr Arg Pro Asn Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro
 1 5 10 15

Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr Ile Arg Gln
 20 25 30

Ala His Cys
 35

<210> 4
 <211> 35
 <212> PRT
 <213> Human immunodeficiency virus type 1

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> V3 loop of Thai-E strain of HIV-1

<400> 4
 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Ile Thr Ile Gly Pro
 1 5 10 15

Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp Ile Arg Lys
 20 25 30

Ala Tyr Cys
 35

<210> 5
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:coding strand
of duplex containing novel PstI site

<400> 5
tggccctgac cctggccgccc gccgagagcg agcgcttcgt ccggcagggc accggcaacg 60
acgaggccgg cgccggcaaac ctgcagggcc 90

<210> 6
<211> 24
<212> PRT
<213> Pseudomonas aeruginosa

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Ib loop region of wild-type Pseudomonas exotoxin A

<400> 6
Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala
1 5 10 15
Gly Glu Cys Ala Gly Pro Ala Asp
20

<210> 7
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ib loop region
of ntPE-V34MN14 protein

<400> 7
Gly Ala Ala Asn Leu His Cys Gly Ile His Ile Gly Pro Gly Arg Ala
1 5 10 15
Phe Tyr Thr Thr Lys Cys Met Gln Gly Pro Ala Asp
20 25

<210> 8
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ib loop region
of ntPE-V3MN26 protein

<400> 8
Gly Ala Ala Asn Leu His Cys Asn Tyr Asn Lys Arg Lys Arg Ile His
1 5 10 15

Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr
20 25 30

Ile Cys Met Gln Gly Pro Ala Asp
35 40

<210> 9
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ib loop region
of ntPE-V3Th-E26 protein

<400> 9
Gly Ala Ala Asn Leu His Cys Ser Asn Asn Thr Arg Thr Ser Ile Thr
1 5 10 15

Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp
20 25 30

Asp Ile Cys Met Gln Gly Pro Ala Asp
35 40

<210> 10
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ib loop region
of ntPE-fp16 protein

<400> 10
Gly Ala Ala Asn Leu Gln Cys Arg Leu Glu Glu Lys Lys Gly Asn Tyr
1 5 10 15

Val Val Thr Asp His Arg Leu Cys Leu Gln Gly Pro Ala Asp
20 25 30

<210> 11
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:endoplasmic
reticulum (ER) retention sequence

<400> 11
Arg Glu Asp Leu Lys
1 5

<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: endoplasmic
reticulum (ER) retention sequence

<400> 12
Arg Glu Asp Leu
1

<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: endoplasmic
reticulum (ER) retention sequence

<400> 13
Lys Asp Glu Leu
1